

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 21, 2001, 12:06:13 ; Search time 20.59 Seconds

(without alignments)
924,523 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-486-334-2
1641
1 MATCIDTCRCNTODDDSRF.....IPCITMDQSTYLEMSDYVI 314

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1641	100.0	314	21	AA645802
2	1641	100.0	314	21	AA93901
3	1349	82.2	263	21	AA645803
4	1215	74.0	336	21	AA93903
5	1215	74.0	391	21	AA93904
6	1213	73.9	1772	21	AA652485
7	1213	73.9	1776	21	AA652484
8	1213	73.9	1787	21	AA652483
9	916	55.8	180	21	AA608083
10	880	53.6	286	21	AA444770
11	849.5	51.8	312	21	AA639465

12	849.5	51.8	312	21	AA93902	Amino acid sequenc
13	846.5	51.6	312	21	AA621076	Arabidopsis thalia
14	846	51.6	294	21	AAV44767	Impatiens balsamia
15	831	50.6	303	21	AAV44768	Rice serine O-acet
16	723.5	44.1	224	21	AAV44769	Amino acid sequenc
17	711	43.3	359	21	AA93905	Soybean serine O-a
18	656	40.0	157	21	AAV44771	E. coli serine ace
19	652.5	39.8	273	18	AAW5073	E. coli serine ace
20	648.5	39.5	258	18	AAW5084	E. coli serine ace
21	648.5	39.5	263	18	AAW5083	E. coli serine ace
22	648.5	39.5	263	18	AAW5093	E. coli serine ace
23	648.5	39.5	270	18	AAW5092	E. coli serine ace
24	648.5	39.5	271	18	AAW5091	E. coli serine ace
25	648.5	39.5	273	13	AAW3780	E. coli serine tran
26	648.5	39.5	273	18	AAW5074	E. coli serine ace
27	648.5	39.5	273	18	AAW5075	Wild type Escheric
28	648.5	39.5	273	18	AAW5076	Protein encoded by
29	648.5	39.5	273	20	AAV3827	Escherichia coli s
30	648.5	39.5	273	21	AAV57823	Escherichia coli s
31	646.5	39.4	273	18	AAW5070	E. coli serine ace
32	645.5	39.3	273	18	AAW5078	E. coli serine ace
33	645	39.3	253	21	AAV57826	Escherichia coli s
34	644	39.2	253	21	AAV57827	Escherichia coli s
35	643.5	39.2	257	18	AAW5085	E. coli serine ace
36	643.5	39.2	273	18	AAW5075	E. coli serine ace
37	643.5	39.2	273	18	AAW5077	E. coli serine ace
38	642.5	39.2	273	18	AAW5071	E. coli serine ace
39	642.5	39.2	273	18	AAW5068	E. coli serine ace
40	642	39.1	259	21	AAW5084	Arabidopsis thalia
41	642	39.1	253	21	AAV57830	Escherichia coli s
42	641.5	39.1	273	18	AAW5082	E. coli serine ace
43	641.5	39.1	273	18	AAW5069	E. coli serine ace
44	641	39.1	253	21	AAV57831	Escherichia coli s
45	640.5	39.0	175	21	AAV44765	Corn serine O-acet

ALIGNMENTS

RESULT	1
AA645802	AA645802 standard; Protein; 314 AA.
AC	AA645802;
XX	18-OCT-2000 (first entry)
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 57548.
XX	Protein identification; signal transduction pathway; metabolic pathway;
XX	hybridisation assay; genetic mapping; gene expression control; promoter;
XX	termination sequence.
XX	Arabidopsis thaliana.
OS	EP1033405-A2.
PN	06-SEP-2000.
XX	25-FEB-2000; 2000EP-0301439.
PF	25-FEB-1999; 9905-0121825.
XX	05-MAR-1999; 9905-0123180.
PR	09-MAR-1999; 9905-0123548.
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 Db 1 matcidtctrtgntqddsrffcciknffrpgfsvnrkikhgqiedddvwlkmlleaksdv 60
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 Db 61 kgepllsnyyastshrslesalahlsvklslnlpntlfeleltsyleespetieest 120
 QY 121 KODLIWVERDPACISYVHCFEGKFLACQAHRIATHLMKONRKIVALLIONRVSSEFA 180
 Db 121 kqdlwverdpacisylvhcfegkflacqahriahtlwkgnrkivaalllgnrvsesfa 180
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 Db 181 vdihpgakigkglldhagvvyigetavvgdnvsilhgvtlgctgkgsqdrhpkigdgvl 240
 QY 241 IGAGSCITGNITIGEGAKIGSGSVVVKDVPARTAVGNPARLIGKRNPRKHDKIPCLTM 300
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 QY 301 DQTSYLEWSDYVI 314
 Db 301 dqtsylewsdyvi 314

RESULT 2

AAV93901 standard; Protein; 314 AA.

AAV93901;

03-OCT-2000 (first entry)

DE Amino acid sequence of serine acetyltransferase (SAT) isoform SAT3.
 XX Serine acetyltransferase; SAT; SAT3; transgenic plant; cysteine;
 KW glutathione; methionine; nutrient value; plant-derived food;
 XX glutathione; viral resistance.

XX Arabidopsis thaliana.

PN W0200036127-A1.

XX *22-JUN-2000.

XX 17-DEC-1999; 99WO-FR03179.

XX 17-DEC-1998; 98FR-0016163.
 XX (AVER) AVENTIS CROPPSCIENCE SA.
 PA Droux M, Lappartient A, Derosé R, Job D;
 PI WPI; 2000-431603/37.
 DR N-PSDB; AAA47173.

PT Increasing production of sulfur-containing compounds, e.g. cysteine or
 PT methionine, in plants, useful e.g. for improving nutritional value, by
 PT overexpressing serine acetyltransferase

PS Claim 9; Page 50-51; 69pp; French.

CC The present sequence represents an isoform of serine acetyltransferase
 CC (SAT). The SAT polynucleotide is used to produce transgenic plants,
 CC which have increased production of cysteine, glutathione, methionine
 CC and their sulfur-containing derivatives. SAT catalyses conversion of
 CC serine to O-acetylsulfonamide which is a precursor (by reaction with sulphide)
 CC for cysteine, itself a precursor for the other sulphur-containing
 CC compounds. The SAT polynucleotides and polypeptides are used to improve
 CC the nutrient value of plant-derived foods, and also (associated with
 CC increased production of glutathione) to improve resistance to stress.

SQ Sequence 314 AA:

Query Match 100.0%; Score 1641; DB 21; Length 314;
 Best Local Similarity 100.0%; Pred. No. 2e-151;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATCIDTCRTGNTODDSRFCCIKNFRPGFSVNRKIHHTQIEDDDVWIKMLEAKSDV 60
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 QY 61 KOEPLISNYVASTSHRSLESALAHILSVKLSNLPNTLFELETSYLESPETIEEST 120
 Db 61 kgepllsnyyastshrslesalahlsvklslnlpntlfeleltsyleespetieest 120
 QY 121 KODLIWVERDPACISYVHCFEGKFLACQAHRIATHLMKONRKIVALLIONRVSSEFA 180
 Db 121 kqdlwverdpacisylvhcfegkflacqahriahtlwkgnrkivaalllgnrvsesfa 180
 QY 181 VDIHPGAKIGKGLLDHAGVYIGETAVVGDVNSILHGVTLGCTGKOSGDRHPKIGDGL 240
 Db 181 vdihpgakigkglldhagvvyigetavvgdnvsilhgvtlgctgkgsqdrhpkigdgvl 240
 QY 241 IGAGSCITGNITIGEGAKIGSGSVVVKDVPARTAVGNPARLIGKRNPRKHDKIPCLTM 300
 Db 241 igagsciltgnitigegakigsgsvvkvdpartlavgnparl199kenprkhdkipcltm 300
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 Db 301 dqtsylewsdyvi 314

RESULT 3

AAG45803 standard; Protein; 263 AA.

AAG45803;

18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 57549.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 XX termination sequence.

OS Arabidopsis thaliana.

XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 10-AUG-1999; 99US-0148319.
PR 11-AUG-1999; 99US-0148341.
PR 12-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 13-AUG-1999; 99US-0149368.
PR 16-AUG-1999; 99US-0149175.
PR 17-AUG-1999; 99US-0149426.
PR 18-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151308.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.

PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156599.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 82.2%; Score 1349; DB 21; Length 263;
 Best Local Similarity 100.0%; Pred. NO. 4e-123;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 MLEAKSDVKQEPILSNYYASTSHRSLESALAHILSVKLSNLPSTLFEFLISYLE 111
 DB 1 mleaksdvkgqepilsnyyastshrslesalahilsvklsnlpstlfeffisyle 60
 QY 112 ESPFETESTKODLAVKRPDPACISYVHCFLEKGFACQAHRIAHILWKONRKIVALLI 171
 DB 61 espfetestkdllavkerdpacisylvhcflekgfllaqhriahclwknrkivalli 120
 QY 172 QNRVSESAVNIHPGAKIGKGIILDHANGVYIGFAVGVNDVSIHLHCVTGGTGKOSGDR 231
 DB 121 qnrveseavnihpgakigkgiilidhaagvviqetavgvndvsihlhgvclggqgdr 180
 QY 232 HPKIGDGVLLIGAGSCILGNITIGEGAKIGSGSVVKKDVPARTTAVGMPARLIGKENPRK 291
 DB 181 hpkgdgvlligagscilgnitigegakigsgsvvkvdparttavgparrligkenprk 240
 QY 292 HDKIPCLTMDOTSYLTWMSDYVI 314
 DB 241 hdkipcltmdqtsyltewsdvyl 263

RESULT 4
 AAY93903
 ID AAY93903 standard; Protein; 336 AA.
 XX
 AC AAY93903;
 XX

DT 03-OCT-2000 (first entry)
 XX
 DE Amino acid sequence of serine acetyltransferase (SAT) isoform SAT1'.
 XX
 KW Serine acetyltransferase; SAT; SAT1'; transgenic plant; cysteine;
 KW glutathione; methionine; nutrient value; plant-derived food;
 KW glutathione; viral resistance.
 XX
 OS Arabidopsis thaliana.
 XX
 PN W0200036127-A1.
 XX
 PD 22-JUN-2000.
 XX
 PF 17-DEC-1999; 99WO-FR03179.
 XX
 PR 17-DEC-1998; 98FR-0016163.
 XX
 PA (AVET) AVENTIS CROPS SCIENCE SA.
 XX
 PI Dröux M, Lappartient A, Derose R, Job D;
 XX
 DR WPI: 2000-431603/37.
 DR N-PSDB; AAA47175.
 XX
 PT Increasing production of sulfur-containing compounds, e.g. cysteine or
 PT methionine, in plants, useful e.g. for improving nutritional value, by
 PT overexpressing serine acetyltransferase
 XX
 PS Claim 14; Page 53-54; 69pp; French.

The present sequence represents an isoform of serine acetyltransferase (SAT). The SAT polynucleotide is used to produce transgenic plants, which have increased production of cysteine, glutathione, methionine and their sulfur-containing derivatives. SAT catalyses conversion of serine to O-acetylsertine which is a precursor (by reaction with sulphide) for cysteine, itself a precursor for the other sulphur-containing compounds. The SAT polynucleotides and polypeptides are used to improve the nutrient value of plant-derived foods, and also (associated with increased production of glutathione) to improve resistance to stress.

SO Sequence 336 AA;

Query Match 74.0%; Score 1215; DB 21; Length 336;
 Best Local Similarity 72.0%; Pred. No. 6.2e-10;
 Matches 242; Conservative 31; Mismatches 41; Indels 22; Gaps 4;

QY 1 MARCITDTCRGNTQ-----DDSRPCCIKNFFRCPS---VNRKIHHTQ--IFD 44
 DB 1 maacitdctcrgkqpsprdsakhddesqfrymnyfrp:ressfngtqkcltrplled 60
 QY 45 -----DDDWIKMLEAKSDVKQEPILSNYYASTSHRSLESALAHILSVKLSNLP 98
 DB 61 lddaevdvwaklreesaadslakepivasaynasivsqrsleaalantlvkslnlhp 120
 QY 99 SNTLFEFLISYLEESPETESTKODLAVKRPDPACISYVHCFLEKGFACQAHRIAHNT 158
 DB 121 sntlfeffisylvleespetestkdllavkerdpacisylvhcflekgfllaqhriahe 180
 QY 159 LMKONRKIVALLIQNRVSESAVNIHPGAKIGKGIILDHCVIGETAVGVNDVSIHLG 218
 DB 181 lwcqdrkllallilqnrveseafavdfrpakiqtlldhna:alvigelavgvnvsilhn 240
 QY 219 VTLGGTGKOSGDRHPKIGGVLLIGAGSCILGNITIGEGAKIGSGSVVKKDVPARTTAVGN 278
 DB 241 vtlggtgkgcgdrhpkiggvlligagscilgnitigegakigsgsvvkvdparrtavgn 300
 QY 279 PARLIGKENPRKHDKIPCLTMDOTSYLTWMSDYVI 314
 DB 301 parligkenprkhdkipcltmdqtsyltewsdvyl 336

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RESULT 5
AA93904
ID AA93904 standard; Protein; 391 AA.
XX
XX AA93904;
XX
DT 03-OCT-2000 (first entry)
XX
DE Amino acid sequence of serine acetyltransferase (SAT) isoform SAT1.
XX
XX Serine acetyltransferase; SAT; SAT1; transgenic plant; cysteine;
XX glutathione; methionine; nutrient value; plant-derived food;
XX glutathione; viral resistance.
XX
XX Arabidopsis thaliana.
XX
XX Key Location/Qualifiers
XX Peptide 1..63
XX FT /note="signal peptide"
XX FT
XX
XX MO200036127-A1.
XX
XX 22-JUN-2000.
XX
XX 17-DEC-1999; 99WO-FR03179.
XX
XX 17-DEC-1998; 98FR-0016163.
XX
XX (AVET) AVENTIS CROPS SCIENCE SA.
XX
XX Droux M, Lapartient A, Derose R, Job D;
XX
XX WPI: 2000-431603/37.
XX N-RSDB; AAA47176.
XX
XX Increasing production of sulfur-containing compounds, e.g. cysteine or
XX methionine, in plants, useful e.g. for improving nutritional value, by
XX overexpressing serine acetyltransferase
XX
XX Disclosure; Page 54-56; 6pp; French.
XX
XX The present sequence represents an isoform of serine acetyltransferase
XX (SAT). The SAT polynucleotide is used to produce transgenic plants,
XX which have increased production of cysteine, glutathione, methionine
XX and their sulfur-containing derivatives. SAT catalyses conversion of
XX serine to O-acetylserine which is a precursor (by reaction with sulphide)
XX for cysteine, itself a precursor for the other sulphur-containing
XX compounds. The SAT polynucleotides and polypeptides are used to improve
XX the nutrient value of plant-derived foods, and also (associated with
XX increased production of glutathione) to improve resistance to stress.
XX
XX Sequence 391 AA:

Query Match 74.0%; Score 1215; DB 21; Length 391;
Best Local Similarity 72.0%; Pred. No. 7, 7e-110;
Matches 242; Conservative 31; Mismatches 41; Indels 22; Gaps 4:

QY 1 MACTIDRCRTGNTQ-----DDSRRCCKNFRFGFS---VNRKIHHTQ--IED 44
Db 56 maacidrcrtgkqpsiprdsckhndesgrtymyfrpdrsfngtqkclhtrplld 115
QY 45 -----DDDVWIKLEAKSDVQEPILSNVYVASTSHRSLESALHLVSLNLP 98
Db 116 lidaedvdrwaktreakedkdiakpivasyhasivsgsleaalantlsvlnlnlp 175
QY 99 SNTLFEFLVLESEPIITSTKODLIAYKERDPACISYVHCLGKGLACQAHNIAT 158
Db 176 snlfdlfsvglgnpdlivesvklidlavkerpaciisyhclhikgflacgahiahe 235
QY 159 LMKONRKIVALLIONRVSSEFAVDHPGAKIGKIGLLDHAFTGVIGETLVAGNVSLILG 218
Db 236 lwtgdrkilaalignrvesafavdhpagakigcigllldhataivigetavgnvslilm 295
```

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QY 219 VTLGGTGKSGDRRHKRTGIDGVLIGAGSCIIINTIGEGAT JSGSVYKDVPAATTAVGN 278
Db 296 vtlggtrgqcgdrhpkigdvvlisagtcilignltlgesak jagsvvlkdvprttavgn 355
QY 279 PARLIGKKNPKRKHKIPCLTMDQTSYLTWSDYVI 31-
Db 356 parllgskdnpkthdkipglmdqtshtshsewsdyvi 393

RESULT 6
AA952485
ID AA952485 standard; Protein; 1772 AA.
XX
XX AA952485;
XX
XX 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 66722.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 28-APR-1999; 99US-0130891.
XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.
XX 04-MAY-1999; 99US-0132484.
XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 06-MAY-1999; 99US-0132487.
XX 07-MAY-1999; 99US-0132863.
XX 11-MAY-1999; 99US-0134256.
XX 14-MAY-1999; 99US-0134218.
XX 14-MAY-1999; 99US-0134219.
XX 14-MAY-1999; 99US-0134221.
XX 14-MAY-1999; 99US-0134370.
XX 18-MAY-1999; 99US-0134376.
XX 19-MAY-1999; 99US-0134941.
XX 20-MAY-1999; 99US-0135124.
XX 21-MAY-1999; 99US-0135353.
XX 24-MAY-1999; 99US-0136269.
XX 25-MAY-1999; 99US-0136021.
XX 27-MAY-1999; 99US-0136392.
XX 28-MAY-1999; 99US-0136782.
XX 01-JUN-1999; 99US-0137222.
XX 03-JUN-1999; 99US-0137528.
XX 04-JUN-1999; 99US-0137502.
XX 07-JUN-1999; 99US-0137724.
XX 08-JUN-1999; 99US-0138094.
XX 10-JUN-1999; 99US-0138540.
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Db 41 maacldtcrtgkqisprdeskhhdessgfrmyfrypdrssingrtcklhrtrplled 100
OY 45 -----DDDWIMKLEAKSDVKOEPLISNYYVASTISHRLESEALHITLSEKLSNENLP 98
Db 101 ldtadavddwakiireaksdiakeplivsaaynasivsqslseaalantlsvklsnlnlp 160
OY 99 SNTLFELFISVLESEPEIISTKODLIVAKERDPACISYVHCFLGFKGLACQAHRIAMT 158
Db 161 sntlfelsgvlgnpivesvklidlavkerdpacisynhcfihfkglacqahriahe 220
OY 159 LKQONKRIYALLIQNRSESAVDIHGAKIGKGIILDHAGVIGFAVGVGDVNSILHG 218
Db 221 lwtcdtrkilaillqnrseefavfnpgaklglgilldhataivgelavvgnvslhln 280
OY 219 VTIIGTGTGQSGDRHPKIGDGVILGAGSCILGNITIGEGAKIGSGSVVKKDVPARTTAVGN 278
Db 281 vtiigrtgkqgdtrhpkiqgdvlllgagtcilgnitlgsegaklgagvsvlkdvprrtlavgn 340
OY 279 PARLIGKENPRKHDKITPCLTMDOTSYLTWMSDYVI 314
Db 341 parllgqknhpkthdklpgltdqtlshsewsdyiv 376
RESULT 7
AAG52484
ID AAG52484 standard; Protein; 1776 AA.
XX AAG52484;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SFO ID NO: 66721.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 990S-0121825.
PR 05-MAR-1999; 990S-0123180.
PR 09-MAR-1999; 990S-0123548.
PR 23-MAR-1999; 990S-0125788.
PR 25-MAR-1999; 990S-0126264.
PR 29-MAR-1999; 990S-0126785.
PR 01-APR-1999; 990S-0127462.
PR 06-APR-1999; 990S-0128234.
PR 08-APR-1999; 990S-0128714.
PR 16-APR-1999; 990S-0129845.
PR 19-APR-1999; 990S-0130077.
PR 21-APR-1999; 990S-0130449.
PR 23-APR-1999; 990S-0130510.
PR 28-APR-1999; 990S-0130891.
PR 30-APR-1999; 990S-0131449.
PR 30-APR-1999; 990S-0132048.
PR 30-APR-1999; 990S-0132407.
PR 04-MAY-1999; 990S-0132484.
PR 05-MAY-1999; 990S-0132485.
PR 06-MAY-1999; 990S-0132486.
PR 06-MAY-1999; 990S-0132487.
PR 07-MAY-1999; 990S-0132863.
PR 11-MAY-1999; 990S-0134256.
PR 14-MAY-1999; 990S-0134218.
PR 14-MAY-1999; 990S-0134219.
PR 14-MAY-1999; 990S-0134221.
PR 14-MAY-1999; 990S-0134370.
PR 18-MAY-1999; 990S-0134768.

PR 19-MAY-1999; 990S-0134941.
PR 20-MAY-1999; 990S-0135124.
PR 21-MAY-1999; 990S-0135353.
PR 24-MAY-1999; 990S-0135629.
PR 25-MAY-1999; 990S-0136021.
PR 27-MAY-1999; 990S-0136392.
PR 28-MAY-1999; 990S-0136782.
PR 01-JUN-1999; 990S-0137222.
PR 03-JUN-1999; 990S-0137528.
PR 04-JUN-1999; 990S-0137502.
PR 07-JUN-1999; 990S-0137724.
PR 08-JUN-1999; 990S-0138094.
PR 10-JUN-1999; 990S-0138540.
PR 10-JUN-1999; 990S-0138847.
PR 14-JUN-1999; 990S-0139119.
PR 16-JUN-1999; 990S-0139452.
PR 16-JUN-1999; 990S-0139453.
PR 17-JUN-1999; 990S-0139452.
PR 18-JUN-1999; 990S-0139454.
PR 18-JUN-1999; 990S-0139455.
PR 18-JUN-1999; 990S-0139456.
PR 18-JUN-1999; 990S-0139457.
PR 18-JUN-1999; 990S-0139458.
PR 18-JUN-1999; 990S-0139459.
PR 18-JUN-1999; 990S-0139460.
PR 18-JUN-1999; 990S-0139461.
PR 18-JUN-1999; 990S-0139462.
PR 18-JUN-1999; 990S-0139463.
PR 18-JUN-1999; 990S-0139750.
PR 18-JUN-1999; 990S-0139763.
PR 21-JUN-1999; 990S-0139817.
PR 22-JUN-1999; 990S-0139899.
PR 23-JUN-1999; 990S-0140353.
PR 24-JUN-1999; 990S-0140354.
PR 24-JUN-1999; 990S-0140695.
PR 28-JUN-1999; 990S-0140823.
PR 29-JUN-1999; 990S-0140931.
PR 30-JUN-1999; 990S-0141287.
PR 01-JUL-1999; 990S-0141842.
PR 01-JUL-1999; 990S-0142154.
PR 02-JUL-1999; 990S-0142055.
PR 06-JUL-1999; 990S-0142390.
PR 08-JUL-1999; 990S-0142803.
PR 09-JUL-1999; 990S-0142920.
PR 12-JUL-1999; 990S-0142977.
PR 13-JUL-1999; 990S-0143542.
PR 14-JUL-1999; 990S-0143624.
PR 15-JUL-1999; 990S-0144005.
PR 16-JUL-1999; 990S-0144085.
PR 16-JUL-1999; 990S-0144086.
PR 19-JUL-1999; 990S-0144335.
PR 19-JUL-1999; 990S-0144331.
PR 19-JUL-1999; 990S-0144332.
PR 19-JUL-1999; 990S-0144333.
PR 19-JUL-1999; 990S-0144334.
PR 19-JUL-1999; 990S-0144335.
PR 20-JUL-1999; 990S-0144332.
PR 20-JUL-1999; 990S-0144884.
PR 21-JUL-1999; 990S-0144814.
PR 21-JUL-1999; 990S-0145086.
PR 21-JUL-1999; 990S-0145087.
PR 21-JUL-1999; 990S-0145088.
PR 22-JUL-1999; 990S-0145089.
PR 22-JUL-1999; 990S-0145192.
PR 22-JUL-1999; 990S-0145193.
PR 23-JUL-1999; 990S-0145218.
PR 23-JUL-1999; 990S-0145224.
PR 26-JUL-1999; 990S-0145276.
PR 27-JUL-1999; 990S-0145913.
PR 27-JUL-1999; 990S-0145918.
PR 27-JUL-1999; 990S-0145919.

21 APR-1999; 99US-0130449.
23-APR-1999; 99US-0130510.
23-APR-1999; 99US-0130891.
28-APR-1999; 99US-0131140.

PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160981.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161933.
PR 29-OCT-1999; 99US-0162142.

Query Match 73.9%; Score 1213; DB 21; Length 1787;
Best Local Similarity 71.4%; Pred. No. 1,1e-108;
Matches 240; Conservative 33; Mismatches 41; Indels 22; Gaps 4;

QY 1 MATCIDTCRTGNTQ-----DDDSRRCIKNFRPGFS---VNRKIHHTQ--TED 44
Db 56 maacldtrctgkpsprdsakhdhesgfrymnyftrpdrsfngtqtklhrpiled 115
QY 45 -----DDDWIKMLEAKSDVKOEPILSNYYASTSHRSLSALAHISVKLSNLP 98
Db 116 ldrdaevdvavaklireakeplvayhasivsgtslaalantlsvkslnlp 175
QY 99 SNTLFELISVLESPETIEESTKODIAKEPRPACISYHCHLIGRGTACCAHRIAH 158
Db 176 sntlfelisyvlgpdpdvayekidllavkerdpacisvychlthfkgflacqahriahe 235
QY 159 LMKONRKIVALLIQNRVSESAVNDIHPGAKIGKIGLIDHATGVIGETAVGVNDVSTLHG 218
Db 236 lwtgdrkiallignrveafavdfrhpgakigtgllidhatavlgetavgvnvsllhm 295
QY 219 VTLGCTGOSGDHPKIGDGVILIGASCLIGNITIEGAKIGSGSVVVKDVPARTTAVGN 278
Db 296 vtlgctgagcdgdrhpkigdgvgitccllgnlillegakigsgsvvklkdvprttaavn 355
QY 279 PARLIGKENRKHDKIPCLTMDQTSYLTMSDYVI 314
Db 356 parllgqkdpkndkplglmdqtslshsawdyiv 391

RESULT 9

AAG08083 standard; Protein; 180 AA.

AAG08083;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 5483.

KW Protein identification: signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

PN EP103405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.
PR 22-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
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 PR 29-OCT-1999; 99US-0162142.

Query Match 55.8%; Score 916; DB 21; Length 180;
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 D 1 matchhcrtrgtqdddsrffcciknfrpgfsvnrkrihtqiedddvwmkmeesdv 60
 QY 61 KQEPILSNYYASTSHSLESAHLIIIVKXISNMLPSNTJELPFSVYESPEIEST 120
 D 61 kqepilsnyyastshslesahlilsvkxlnlpsntlfelffsveespettest 120
 QY 121 KODIIAVERDPACISYVHCFEGFKFLACQAHRIAHITLKKONRKIVALLIQRVSSFA 180
 D 121 kqdliaverdpacisylvhcfefgfkflacqahriahitlwnqnrkivaalligrvssfa 180

RESULT 10
 ID AAY44770
 AAY44770 standard; Protein; 286 AA.
 XX AAY44770;
 AC AAY44770;
 XX 04-MAY-2000 (first entry)
 DT
 XX
 DE Soybean serine O-acetyltransferase-1.
 XX
 KW Serine O-acetyltransferase; sulphate assimilation; O-acetylserine;
 KW soybean; clone srl.pK0162.49; cysteine formation; marker; probe;
 KW plant breeding; transgenic plant.
 XX
 OS Glycine max.
 XX
 PN WO200004167-A2.
 XX
 XX 27-JAN-2000.
 PD
 XX 13-JUL-1999; 99WO-US15872.
 PF
 XX 14-JUL-1999; 98US-0092833.

18-JUN-1999; 99US-0139750.
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	Query Match	51.68;	Score	846.5;	DB	21;	Length	312;	
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	Matches	160;	Conservative	44;	Mismatches	63;	Indels	1;	Gaps
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Dd	45	Iwqgikaeardraadeapalasyllstlshslestersfblgnkicssltlsclyldfl	104						
QY	108	SVEESEPEIESTKODLIIVAKERDPACISVYHCFLGFGKFLAQQAHRIATLMKNRKIV	167						
Dd	105	nftsdpslnmatvadriaavxvropacsfbhcllnygfialghrvshklwtgsrkpl	164						
QY	168	ALLIQNRSESFADIDHGARKIGKILLDHATGVIGELVVGDNVSILHCVLTGGTGKO	227						
Dd	165	alaahstistdfavrdhpakikgilldhagvvayvefnygnvslilhvcllggtgka	224						
QY	228	SGDRHPRTGDVLVLAGSCIIIGNITIGEGAKTGSVVVFHWARTAVGNPARILIGKE	287						
Dd	225	cgdthnpktygdgcilgaagatllgnvxigagaxkgagsvvlpypcrgtavgnparilvygke	284						
QY	288	NPRKHD-KIPCLIMDOTSYLTMSDVI	314						
Dd	285	kptlhdeecpgesmdhtsfisewsdyl	312						

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OY 164 KRIVALLIONRYSSESPAVDIHPGAKIGKGIILDHATGVVIGETAVVGDVNSILHGVTLLG 223
Db 157 rralalalqsrvaevfaavdihpaalqkgyllldhetgavlgetavgdnvsihhvcllg 216
OY 224 TKGOSGDRHPRKIGDGYLIGAGSCITGNITIGEGAKIGSGSVVYKDVPAFTTAVGNPARLI 283
Db 217 tskavagdrhpkigdyvlligagatlignvrigagakiagslivildvprltcavgnparli 276
OY 284 GKENPRKHDKTPCLTMDOTSYLTWSDYVI 314
Db 277 gqk---kgdmpgesmdhtsfiqwsdysi 303
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